

AMENDMENTS TO THE CLAIMS

Please cancel claims 2-3, 5-10 and 22-49.

Please amend claims 1, 4, 11-21, and 50-52 and add new claim 53 as shown in the following list of claims.

1. (Currently Amended) An i[[I]]solated polynucleotide[[s]] coding for a ferroportin 1 polypeptide comprising mutated in one of the following amino acids:

-amino acid at position 80 of SEQ ID NO:2, wherein the glycine at position 80 of SEQ ID NO:2 is substituted with a serine.

-amino acid at position 174 of SEQ ID NO:2;

-amino acid at position 248 of SEQ ID NO:2, as compared to the wild type sequence.

2-3. (Canceled).

4. (Currently Amended) The isolated p[[P]]olynucleotide according to claim 1 [[3]] comprising SEQ ID NO:1, wherein nucleotide 238 of SEQ ID NO:1 is characterized in that said polymorphism is a substitution of a G with an A.

5-10. (Canceled).

11. (Currently Amended) The isolated p[[P]]olynucleotide according to claim 1, wherein said isolated polynucleotide characterized in that it is genomic DNA.

12. (Currently Amended) The isolated p[[P]]olynucleotide according to claim 1, wherein said isolated polynucleotide characterized in that it is mRNA.

13. (Currently Amended) The isolated p[[P]]olynucleotide according to claim 1, wherein said isolated polynucleotide characterized in that it is cDNA.

14. (Currently Amended) The isolated p[[P]]olynucleotide coding for a mutated ferroportin 1 according to claim 1, wherein the characterized in that its nucleotide sequence of said isolated polynucleotide is corresponds to SEQ ID NO:3, 5, or 7.

15. (Currently Amended) An isolated p[[P]]olynucleotide comprising more than carrying at least 10 consecutive nucleotides derived from any one of sequences SEQ ID NO:3, 5, or 7, and characterized by comprising at least one of polymorphic nucleotides respectively selected from the group consisting of:

- wherein the isolated polynucleotide comprises polymorphism corresponding to position 238 of SEQ ID NO:3;
- polymorphism corresponding to position 521 of SEQ ID NO:5, or
- polymorphism corresponding to position 744 of SEQ ID NO:7.

16. (Currently Amended) The isolated p[[P]]olynucleotide according to claim 15 characterized by further comprising at least one of the oligonucleotides corresponding to sequences of SEQ ID NO: 13 or 14, 9-27.

17. (Currently Amended) An isolated p[[P]]olynucleotide having a complementary sequence complementary as compared to the polynucleotide according to claim 15.

18. (Currently Amended) The isolated p[[P]]olynucleotide according to claim 1 comprising a label, characterized in that it is labelled.

19. (Currently Amended) A r[[R]]ecombinant vector characterized by comprising the isolated polynucleotide according to claim 1.

20. (Currently Amended) An i[[I]]solated cell characterized in that it is transfected or transformed with the recombinant vector according to claim 19.

21. (Currently Amended) A e[[E]]ukaryotic cell, tissue or non-human animal including a transgene, wherein such transgene is at least one isolated[[a]] polynucleotide according to claim 1.

22-49. (Canceled).

50. (Currently Amended) A k[[K]]it for the non-HFE hereditary Hemochromatosis diagnosis comprising at least one ~~the isolated polynucleotide of the oligonucleotides~~ according to claim 1.

51. (Currently Amended) A k[[K]]it for hereditary impaired iron homeostasis diagnosis comprising at least one ~~the isolated of the~~ polynucleotide[[s]] according to claim 1.

52. (Currently Amended) A k[[K]]it for detecting a polymorphism selected from the group consisting of: polymorphism of nucleotide ~~corresponding to~~ position 238 of SEQ ID NO: 1, ~~polymorphism of the nucleotide corresponding to position 521 of SEQ ID NO: 1, polymorphism of the nucleotide corresponding to position 744 of SEQ ID NO: 1 characterized by~~ comprising at least one of the oligonucleotides of sequence: SEQ ID NO: 13, ~~or 14, 19 or 20~~ optionally in combination with TspR1 ~~at least one of the following restriction enzymes: TspR1, BsmI, PvuII.~~

53. (New) The isolated polynucleotide according to claim 15 or 17 comprising between 15 and 50 consecutive nucleotides.